

D. Romea



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/592,685

DATE: 05/21/2002

TIME: 14:17:18

Input Set : N:\Crf3\RULE60\09592685.raw

Output Set: N:\CRF3\05212002\I592685.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bonadio, Jeffrey

6 Yin, Wushan

.8 (ii) TITLE OF INVENTION: LATENT TGF(BINDING PROTEIN (LTBP)

9 GENES, COMPOSITIONS AND METHODS

11 (iii) NUMBER OF SEQUENCES: 13

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Williams, Morgan & Amerson

15 (B) STREET: 7676 Hillmont, Suite 250

16 (C) CITY: Houston

17 (D) STATE: Texas

18 (E) COUNTRY: USA

19 (F) ZIP: 77040

ENTERED

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/592,685

C--> 29 (B) FILING DATE: 12-Jun-2000

30 (C) CLASSIFICATION:

45 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/479,722B

34 (B) FILING DATE: 07-JUN-1995

38 (A) APPLICATION NUMBER: US PCT/US95/02251

39 (B) FILING DATE: 21-FEB-1995

42 (A) APPLICATION NUMBER: US 08/316,650

43 (B) FILING DATE: 30-SEP-1994

46 (A) APPLICATION NUMBER: US 08/199,780

47 (B) FILING DATE: 18-FEB-1994

49 (viii) ATTORNEY/AGENT INFORMATION:

50 (A) NAME: Fussey, Shelley P.M.

51 (B) REGISTRATION NUMBER: 39,458

52 (C) REFERENCE/DOCKET NUMBER: 4100.000500/FUS

54 (ix) TELECOMMUNICATION INFORMATION:

55 (A) TELEPHONE: (713) 934-7000

56 (B) TELEFAX: (713) 934-7011

59 (2) INFORMATION FOR SEQ ID NO: 1:

61 (i) SEQUENCE CHARACTERISTICS:

62 (A) LENGTH: 5499 base pairs

63 (B) TYPE: nucleic acid

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64          (C) STRANDEDNESS: single
65          (D) TOPOLOGY: linear
W--> 67      (ii) MOLECULE TYPE:
68          (A) DESCRIPTION: /desc = "DNA"
70      (ix) FEATURE:
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 1..5499
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 ATG GAG AGC ACC TCC CCG CGA GGT CTC CGG TGC CCA CAG CTC TGC AGC      48
77 Met Glu Ser Thr Ser Pro Arg Gly Leu Arg Cys Pro Gln Leu Cys Ser
78   1           5           10           15
80 CAC TCT GGC GCC ATG AGA GCG CCG ACC ACC GCT CGC TGC TCC GGA TGC      96
81 His Ser Gly Ala Met Arg Ala Pro Thr Thr Ala Arg Cys Ser Gly Cys
82           20           25           30
84 ATC CAA CGG GTG CGT TGG AGG GGC TTC CTG CCA CTT GTC CTG GCT GTC      144
85 Ile Gln Arg Val Arg Trp Arg Gly Phe Leu Pro Leu Val Leu Ala Val
86   35           40           45
88 TTG ATG GGG ACA AGT CAT GCC CAA CGG GAT TCC ATA GGG AGA TAC GAA      192
89 Leu Met Gly Thr Ser His Ala Gln Arg Asp Ser Ile Gly Arg Tyr Glu
90   50           55           60
92 CCA GCT AGC AGG GAT GCG AAT CGG TTG TGG CAC CCC GTG GGC AGC CAC      240
93 Pro Ala Ser Arg Asp Ala Asn Arg Leu Trp His Pro Val Gly Ser His
94  65           70           75           80
96 CCC GCA GCG GCT GCA GCC AAG GTG TAC AGT CTG TTC CGA GAG CCT GAC      288
97 Pro Ala Ala Ala Ala Ala Lys Val Tyr Ser Leu Phe Arg Glu Pro Asp
98           85           90           95
100 GCG CCG GTC CCC GGC TTG TCG CCC TCT GAG TGG AAC CAG CCG GCC CAG      336
101 Ala Pro Val Pro Gly Leu Ser Pro Ser Glu Trp Asn Gln Pro Ala Gln
102           100           105           110
104 GGG AAC CCG GGA TGG CTC GCA GAG GCC GAG GCC AGG AGG CCA CCT CGA      384
105 Gly Asn Pro Gly Trp Leu Ala Glu Ala Glu Ala Arg Arg Pro Pro Arg
106           115           120           125
108 ACC CAG CAG CTG CGT CGA GTC CAG CCA CCT GTC CAG ACT CGG AGA AGC      432
109 Thr Gln Gln Leu Arg Arg Val Gln Pro Pro Val Gln Thr Arg Arg Ser
110           130           135           140
112 CAT CCC CGG GGC CAG CAG CAG ATA GCA GCC CGG GCT GCA CCT TCT GTC      480
113 His Pro Arg Gly Gln Gln Gln Ile Ala Ala Arg Ala Ala Pro Ser Val
114 145           150           155           160
116 GCG CGC CTG GAA ACC CCT CAG CGA CCC GCG GCT GCA CGG CGA GGG CGG      528
117 Ala Arg Leu Glu Thr Pro Gln Arg Pro Ala Ala Ala Arg Arg Gly Arg
118           165           170           175
120 CTC ACT GGG AGA AAT GTC TGC GGG GGA CAG TGC TGC CCA GGA TGG ACA      576
121 Leu Thr Gly Arg Asn Val Cys Gly Gly Gln Cys Cys Pro Gly Trp Thr
122           180           185           190
124 ACA TCA AAC AGC ACC AAC CAC TGT ATC AAA CCT GTG TGT CAG CCT CCC      624
125 Thr Ser Asn Ser Thr Asn His Cys Ile Lys Pro Val Cys Gln Pro Pro
126           195           200           205
128 TGT CAG AAC CGA GGC TCC TGC AGC AGG CCC CAG GTC TGC ATC TGC CGT      672
129 Cys Gln Asn Arg Gly Ser Cys Ser Arg Pro Gln Val Cys Ile Cys Arg

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130	210	215	220	
132	TCT GGC TTC CGT GGG GCG CGC TGT GAG GAG GTC ATC CCT GAG GAG GAA	720		
133	Ser Gly Phe Arg Gly Ala Arg Cys Glu Glu Val Ile Pro Glu Glu Glu			
134	225 230 235 240			
136	TTT GAC CCT CAG AAT GCC AGG CCT GTG CCC AGA CGC TCA GTG GAG AGA	768		
137	Phe Asp Pro Gln Asn Ala Arg Pro Val Pro Arg Arg Ser Val Glu Arg			
138	245 250 255			
140	GCA CCC GGT CCT CAC AGA AGC AGT GAG GCC AGA GGA AGT CTA GTG ACC	816		
141	Ala Pro Gly Pro His Arg Ser Ser Glu Ala Arg Gly Ser Leu Val Thr			
142	260 265 270			
144	AGA ATA CAG CCG CTG GTA CCA CCA CCA TCA CCA CCT CCA TCT CGG CGC	864		
145	Arg Ile Gln Pro Leu Val Pro Pro Pro Ser Pro Pro Ser Arg Arg			
146	275 280 285			
148	CTC AGC CAG CCC TGG CCC CTG CAG CAG CAC TCA GGG CCG TCC AGG ACA	912		
149	Leu Ser Gln Pro Trp Pro Leu Gln Gln His Ser Gly Pro Ser Arg Thr			
150	290 295 300			
152	GTT CGT CGG TAT CCG GCC ACT GGT GCC AAT GGC CAG CTG ATG TCC AAC	960		
153	Val Arg Arg Tyr Pro Ala Thr Gly Ala Asn Gly Gln Leu Met Ser Asn			
154	305 310 315 320			
156	GCT TTG CCT TCA GGA CTC GAG CTG AGA GAC AGC AGC CCA CAG GCA GCA	1008		
157	Ala Leu Pro Ser Gly Leu Glu Leu Arg Asp Ser Ser Pro Gln Ala Ala			
158	325 330 335			
160	CAT GTG AAC CAT CTC TCA CCC CCC TGG GGG CTG AAC CTC ACC GAG AAA	1056		
161	His Val Asn His Leu Ser Pro Pro Trp Gly Leu Asn Leu Thr Glu Lys			
162	340 345 350			
164	ATC AAG AAA ATC AAA GTC GTC TTC ACC CCC ACC ATC TGC AAG CAG ACC	1104		
165	Ile Lys Lys Ile Lys Val Val Phe Thr Pro Thr Ile Cys Lys Gln Thr			
166	355 360 365			
168	TGT GCC CGG GGA CGC TGT GCC AAC AGC TGT GAG AAG GGT GAC ACC ACC	1152		
169	Cys Ala Arg Gly Arg Cys Ala Asn Ser Cys Glu Lys Gly Asp Thr Thr			
170	370 375 380			
172	ACC TTG TAC AGT CAG GGT GGC CAT GGG CAT GAC CCC AAG TCT GGC TTC	1200		
173	Thr Leu Tyr Ser Gln Gly Gly His Gly His Asp Pro Lys Ser Gly Phe			
174	385 390 395 400			
176	CGT ATC TAT TTC TGC CAA ATC CCC TGC CTG AAT GGT GGC CGC TGC ATC	1248		
177	Arg Ile Tyr Phe Cys Gln Ile Pro Cys Leu Asn Gly Gly Arg Cys Ile			
178	405 410 415			
180	GGC CGG GAC GAG TGC TGG TGT CCA GCC AAC TCC ACA GGA AAG TTC TGC	1296		
181	Gly Arg Asp Glu Cys Trp Cys Pro Ala Asn Ser Thr Gly Lys Phe Cys			
182	420 425 430			
184	CAT CTG CCT GTC CCG CAG CCA GAC AGG GAA CCT GCA GGG CGA GGT TCC	1344		
185	His Leu Pro Val Pro Gln Pro Asp Arg Glu Pro Ala Gly Arg Gly Ser			
186	435 440 445			
188	CGG CAC AGA ACC CTG CTG GAA GGT CCC CTG AAG CAA TCC ACC TTC ACG	1392		
189	Arg His Arg Thr Leu Leu Glu Gly Pro Leu Lys Gln Ser Thr Phe Thr			
190	450 455 460			
192	CTG CCT CTC TCT AAC CAG CTC GCC TCT GTG AAC CCC TCG CTG GTG AAG	1440		
193	Leu Pro Leu Ser Asn Gln Leu Ala Ser Val Asn Pro Ser Leu Val Lys			
194	465 470 475 480			

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196	GTG	CAA	ATT	CAT	CAC	CCG	CCT	GAG	GCC	TCT	GTG	CAG	ATT	CAC	CAG	GTG	1488
197	Val	Gln	Ile	His	His	Pro	Pro	Glu	Ala	Ser	Val	Gln	Ile	His	Gln	Val	
198					485				490						495		
200	GCC	CGG	GTC	CGG	GGT	GAG	CTG	GAC	CCC	GTG	CTG	GAG	GAC	AAC	AGT	GTG	1536
201	Ala	Arg	Val	Arg	Gly	Glu	Leu	Asp	Pro	Val	Leu	Glu	Asp	Asn	Ser	Val	
202				500					505					510			
204	GAG	ACC	AGA	GCC	TCT	CAT	CGC	CCC	CAC	GGC	AAC	CTA	GGC	CAC	AGC	CCC	1584
205	Glu	Thr	Arg	Ala	Ser	His	Arg	Pro	His	Gly	Asn	Leu	Gly	His	Ser	Pro	
206			515					520					525				
208	TGG	GCC	AGC	AAC	AGC	ATA	CCC	GCT	CGG	GCC	GGA	GAG	GCC	CCT	CGG	CCA	1632
209	Trp	Ala	Ser	Asn	Ser	Ile	Pro	Ala	Arg	Ala	Gly	Glu	Ala	Pro	Arg	Pro	
210		530					535					540					
212	CCA	CCA	GTG	CTG	TCT	AGG	CAT	TAT	GGA	CTT	CTG	GGC	CAG	TGT	TAC	CTG	1680
213	Pro	Pro	Val	Leu	Ser	Arg	His	Tyr	Gly	Leu	Leu	Gly	Gln	Cys	Tyr	Leu	
214	545				550				555							560	
216	AGC	ACG	GTG	AAT	GGA	CAG	TGT	GCT	AAC	CCC	CTA	GGT	AGT	CTG	ACT	TCT	1728
217	Ser	Thr	Val	Asn	Gly	Gln	Cys	Ala	Asn	Pro	Leu	Gly	Ser	Leu	Thr	Ser	
218				565					570					575			
220	CAG	GAG	GAC	TGC	TGT	GGC	AGT	GTG	GGG	ACC	TTC	TGG	GGG	GTG	ACC	TCC	1776
221	Gln	Glu	Asp	Cys	Cys	Gly	Ser	Val	Gly	Thr	Phe	Trp	Gly	Val	Thr	Ser	
222			580						585					590			
224	TGT	GCT	CCC	TGC	CCA	CCC	AGA	CAA	GAG	GGT	CCA	GCC	TTC	CCA	GTG	ATT	1824
225	Cys	Ala	Pro	Cys	Pro	Pro	Arg	Gln	Glu	Gly	Pro	Ala	Phe	Pro	Val	Ile	
226			595				600					605					
228	GAA	AAT	GGC	CAG	CTG	GAG	TGT	CCC	CAA	GGA	TAC	AAG	AGA	CTG	AAC	CTC	1872
229	Glu	Asn	Gly	Gln	Leu	Glu	Cys	Pro	Gln	Gly	Tyr	Lys	Arg	Leu	Asn	Leu	
230		610				615						620					
232	AGC	CAC	TGC	CAA	GAT	ATC	AAT	GAG	TGC	CTG	ACC	CTG	GGC	CTC	TGC	AAG	1920
233	Ser	His	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Leu	Thr	Leu	Gly	Leu	Cys	Lys	
234	625				630				635							640	
236	GAC	TCG	GAG	TGC	GTG	AAC	ACC	AGG	GGC	AGC	TAC	CTG	TGC	ACC	TGC	AGG	1968
237	Asp	Ser	Glu	Cys	Val	Asn	Thr	Arg	Gly	Ser	Tyr	Leu	Cys	Thr	Cys	Arg	
238			645						650						655		
240	CCT	GGC	CTC	ATG	CTG	GAT	CCG	TCA	AGG	AGC	CGC	TGC	GTA	TCG	GAC	AAG	2016
241	Pro	Gly	Leu	Met	Leu	Asp	Pro	Ser	Arg	Ser	Arg	Cys	Val	Ser	Asp	Lys	
242			660					665					670				
244	GCT	GTC	TCC	ATG	CAG	CAG	GGA	CTA	TGC	TAC	CGG	TCA	CTG	GGG	TCT	GGT	2064
245	Ala	Val	Ser	Met	Gln	Gln	Gly	Leu	Cys	Tyr	Arg	Ser	Leu	Gly	Ser	Gly	
246			675					680					685				
248	ACC	TGC	ACC	CTG	CCT	TTG	GTT	CAT	CGG	ATC	ACC	AAG	CAG	ATA	TGC	TGC	2112
249	Thr	Cys	Thr	Leu	Pro	Leu	Val	His	Arg	Ile	Thr	Lys	Gln	Ile	Cys	Cys	
250		690				695						700					
252	TGC	AGC	CGT	GTG	GGC	AAA	GCC	TGG	GGT	AGC	ACA	TGT	GAA	CAG	TGT	CCC	2160
253	Cys	Ser	Arg	Val	Gly	Lys	Ala	Trp	Gly	Ser	Thr	Cys	Glu	Gln	Cys	Pro	
254	705				710						715					720	
256	CTG	CCT	GGC	ACA	GAA	GCC	TTC	AGG	GAG	ATC	TGC	CCT	GCT	GGC	CAT	GGC	2208
257	Leu	Pro	Gly	Thr	Glu	Ala	Phe	Arg	Glu	Ile	Cys	Pro	Ala	Gly	His	Gly	
258			725						730						735		
260	TAC	ACC	TAC	TCG	AGC	TCA	GAC	ATC	CGC	CTG	TCT	ATG	AGG	AAA	GCC	GAA	2256

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261	Tyr	Thr	Tyr	Ser	Ser	Ser	Asp	Ile	Arg	Leu	Ser	Met	Arg	Lys	Ala	Glu	
262				740					745					750			
264	GAA	GAG	GAA	CTG	GCT	AGC	CCC	TTA	AGG	GAG	CAG	ACA	GAG	CAG	AGC	ACT	2304
265	Glu	Glu	Glu	Leu	Ala	Ser	Pro	Leu	Arg	Glu	Gln	Thr	Glu	Gln	Ser	Thr	
266			755					760					765				
268	GCA	CCC	CCA	CCT	GGG	CAA	GCA	GAG	AGG	CAA	CCA	CTC	CGG	GCA	GCC	ACC	2352
269	Ala	Pro	Pro	Pro	Gly	Gln	Ala	Glu	Arg	Gln	Pro	Leu	Arg	Ala	Ala	Thr	
270		770					775					780					
272	GCC	ACC	TGG	ATT	GAG	GCT	GAG	ACC	CTC	CCT	GAC	AAA	GGT	GAC	TCT	CGG	2400
273	Ala	Thr	Trp	Ile	Glu	Ala	Glu	Thr	Leu	Pro	Asp	Lys	Gly	Asp	Ser	Arg	
274	785				790				795							800	
276	GCT	GTT	CAG	ATC	ACA	ACC	AGT	GCT	CCC	CAC	CTA	CCT	GCC	CGG	GTA	CCA	2448
277	Ala	Val	Gln	Ile	Thr	Thr	Ser	Ala	Pro	His	Leu	Pro	Ala	Arg	Val	Pro	
278				805					810						815		
280	GGG	GAT	GCC	ACT	GGA	AGA	CCA	GCA	CCA	TCC	TTG	CCT	GGA	CAG	GGC	ATT	2496
281	Gly	Asp	Ala	Thr	Gly	Arg	Pro	Ala	Pro	Ser	Leu	Pro	Gly	Gln	Gly	Ile	
282			820						825					830			
284	CCA	GAG	AGT	CCA	GCA	GAA	GAG	CAA	GTG	ATT	CCC	TCC	AGT	GAT	GTC	TTG	2544
285	Pro	Glu	Ser	Pro	Ala	Glu	Glu	Gln	Val	Ile	Pro	Ser	Ser	Asp	Val	Leu	
286			835				840						845				
288	GTG	ACA	CAC	AGC	CCC	CCA	GAC	TTT	GAT	CCA	TGT	TTT	GCT	GGA	GCC	TCC	2592
289	Val	Thr	His	Ser	Pro	Pro	Asp	Phe	Asp	Pro	Cys	Phe	Ala	Gly	Ala	Ser	
290		850				855						860					
292	AAC	ATC	TGT	GGC	CCT	GGG	ACC	TGT	GTG	AGC	CTC	CCA	AAT	GGA	TAC	AGA	2640
293	Asn	Ile	Cys	Gly	Pro	Gly	Thr	Cys	Val	Ser	Leu	Pro	Asn	Gly	Tyr	Arg	
294	865				870					875					880		
296	TGT	GTC	TGC	AGC	CCT	GGC	TAC	CAG	CTA	CAC	CCC	AGC	CAA	GAC	TAC	TGT	2688
297	Cys	Val	Cys	Ser	Pro	Gly	Tyr	Gln	Leu	His	Pro	Ser	Gln	Asp	Tyr	Cys	
298				885					890						895		
300	ACT	GAT	GAC	AAC	GAG	TGT	ATG	AGG	AAC	CCC	TGT	GAA	GGA	AGA	GGG	CGC	2736
301	Thr	Asp	Asp	Asn	Glu	Cys	Met	Arg	Asn	Pro	Cys	Glu	Gly	Arg	Gly	Arg	
302			900						905					910			
304	TGT	GTC	AAC	AGT	GTG	GGC	TCC	TAC	TCC	TGC	CTC	TGC	TAT	CCT	GGC	TAC	2784
305	Cys	Val	Asn	Ser	Val	Gly	Ser	Tyr	Ser	Cys	Leu	Cys	Tyr	Pro	Gly	Tyr	
306			915				920						925				
308	ACA	CTA	GTC	ACC	CTC	GGA	GAC	ACA	CAG	GAG	TGC	CAA	GAT	ATC	GAT	GAG	2832
309	Thr	Leu	Val	Thr	Leu	Gly	Asp	Thr	Gln	Glu	Cys	Gln	Asp	Ile	Asp	Glu	
310		930				935						940					
312	TGT	GAG	CAG	CCC	GGG	GTG	TGC	AGT	GGT	GGG	CGA	TGC	AGC	AAC	ACG	GAG	2880
313	Cys	Glu	Gln	Pro	Gly	Val	Cys	Ser	Gly	Gly	Arg	Cys	Ser	Asn	Thr	Glu	
314	945				950					955					960		
316	GGC	TCG	TAC	CAC	TGC	GAG	TGT	GAT	CGG	GGC	TAC	ATC	ATG	GTC	AGG	AAA	2928
317	Gly	Ser	Tyr	His	Cys	Glu	Cys	Asp	Arg	Gly	Tyr	Ile	Met	Val	Arg	Lys	
318				965					970						975		
320	GGA	CAC	TGT	CAA	GAT	ATC	AAC	GAA	TGC	CGT	CAC	CCT	GGT	ACC	TGC	CCT	2976
321	Gly	His	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Arg	His	Pro	Gly	Thr	Cys	Pro	
322			980					985						990			
324	GAT	GGG	AGA	TGC	GTC	AAC	TCC	CCT	GGC	TCC	TAC	ACT	TGT	CTG	GCC	TGT	3024
325	Asp	Gly	Arg	Cys	Val	Asn	Ser	Pro	Gly	Ser	Tyr	Thr	Cys	Leu	Ala	Cys	

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:67 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1